

# Solution of a Strongly Coupled Reaction-Diffusion System by the Homotopy Analysis Method

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## Abstract

In this paper, we obtain the analytical solution for a strongly coupled reaction-diffusion system with initial condition by the Homotopy Analysis Method (HAM). The HAM allows for the solution of the strongly coupled reaction-diffusion system to be calculated in the form of an infinite series with components which can be easily calculated. The obtained results are presented and only a few terms are required to obtain an approximate solution that is accurate and efficient.

## 1 Introduction

In this article, the Homotopy Analysis Method (HAM) is used to obtain the approximate solution of a strongly coupled reaction-diffusion system. The system of equations is [7]

$$\begin{cases} u_t = au_{xx} + f(u, v), & 0 < x < 1, \quad 0 < t \leq T \\ v_t = bv_{xx} + g(u, v), & 0 < x < 1, \quad 0 < t \leq T, \\ u(x, 0) = u_0(x), \quad v(x, 0) = v_0(x), & 0 \leq x \leq 1, \\ u_x(0, t) = \alpha_1(t), \quad u_x(1, t) = \beta_1(t), & 0 < t \leq T, \\ v_x(0, t) = \alpha_2(t), \quad v_x(1, t) = \beta_2(t), & 0 < t \leq T, \end{cases} \quad (1.1)$$

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where  $u = u(x, t)$  and  $v = v(x, t)$  are the concentrations of two interacting substances, the constants  $a, b, d$  are such that  $a > 0, d > 0$  and  $b \neq 0$ . The following consistency conditions hold

$$\alpha_1(0) = u'_0(0), \quad \beta_1(0) = u'_0(1), \quad \alpha_2(0) = v'_0(0), \quad \beta_2(0) = v'_0(1).$$

Reaction-diffusion system arises in the study of biology, chemistry, population dynamics [8, 10, 12, 17] and the above system arises in modeling chemical reaction groundwater transport [7]. The global solution of system (1.1) has been investigated by [4, 9, 11, 12, 15, 16]. In [9], Daddiouaissa have considered the condition for existence, uniqueness and boundedness of the global solutions have been found using various technique.

Many non-perturbative methods have been introduced in the literature and these methods have been used to solve applied problems in physics and engineering. Several authors focused on analytical solutions of nonlinear equations by using approximate analytical methods. Example include Yldrm and Momani [18] who applied the homotopy perturbation method (HPM) to fractional oscillator and Koak and Yldrm [19] who solved the 3D Green's function by using HPM. A fractional Zakharov-Kuznetsov equations was solved by Yldrm and Glkanat [20] by using HPM whilst Yldrm et al. [21] used the Modified Variational Iteration Method (MVIM) to solve the Klein-Gordon equation and Raftari and Yldrm [22] found the analytical solution of magneto-hydro-dynamic boundary layer flow of an upper convected Maxwell fluid over a porous stretching sheet by HPM. Analytical solution of generalized Burger and Burger Fisher equations have been obtained by Rashidi and Ganji [23] using HPM and Rashidi and Mohimanian [24] studied the unsteady boundary layer flow and heat transfer due to stretching sheet by HPM. Rashidi and Dinarvand [25] applied the HAM to solve the system of ordinary differential equations.

In this study we aim to apply the HAM to solve the system (1.1). The HAM was developed by Liao [13] who utilized the idea of homotopy in topology. Since then numerous authors have used HAM to solve various differential equations but so far as we are aware not the system (1.1). HAM, as an analytical method, has an advantage over perturbation methods in that it does not depend on small or large parameters. Compared with other analytical methods such as Adomian Decomposition, Variational Iteration Methods, HAM allows for fine-tuning of convergence region and rate of convergence by allowing an auxiliary parameter  $\hbar$  to vary [1, 5]. Compared with numerical methods, it does not require discretization and thus does not have problem of computer round off errors.

Our paper is organized as follows: In section 2, we present a description of the HAM, as expounded by previous researchers in particular [2, 3, 6], applied to the strongly coupled reaction-diffusion system (1.1). In section 3, we employ the HAM for solving strongly coupled reaction-diffusion system and compare the solution obtained with the exact solution. Finally, in section 4, we give the conclusion of this study.

## 2 A description of the HAM for strongly coupled reaction-diffusion system

To apply the HAM, the strongly coupled reaction-diffusion system (1.1) is considered. The following deformation equation was constructed following Liao [13]

$$(1-p)\mathcal{L}_u[\phi(x,t;p) - u_0(x,t)] = p\hbar N_1[\phi(x,t;p)], \quad (2.1)$$

$$(1-p)\mathcal{L}_v[\varphi(x,t;p) - v_0(x,t)] = p\hbar N_2[\varphi(x,t;p)], \quad (2.2)$$

where  $N_1$  and  $N_2$  are two nonlinear operators, whilst  $x$  and  $t$  denote the independent variables.  $p \in [0,1]$  is the embedding parameter,  $\hbar \neq 0$  is an auxiliary parameter and  $u_0(x,t)$  and  $v_0(x,t)$  are, respectively, initial guesses of  $u(x,t)$  and  $v(x,t)$ . The functions  $\phi(x,t;p)$  and  $\varphi(x,t;p)$  are known functions which can be constructed and  $\mathcal{L}_u$  and  $\mathcal{L}_v$  are auxiliary operators that are defined as follows

$$\mathcal{L}_u = \frac{\partial u}{\partial t}, \quad \mathcal{L}_v = \frac{\partial v}{\partial t},$$

and they satisfy

$$\mathcal{L}_u[c_1(x)] = 0, \quad \mathcal{L}_v[c_2(x)] = 0,$$

where  $c_1(x)$  and  $c_2(x)$  are integral constants (partial integration).

When  $p = 0$  and  $p = 1$

$$\phi(x,t;0) = u_0(x,t), \quad \phi(x,t;1) = u(x,t),$$

$$\varphi(x,t;0) = v_0(x,t), \quad \varphi(x,t;1) = v(x,t).$$

As  $p$  increases from 0 to 1, the solution of the strongly coupled reaction-diffusion system (1.1) will vary from the initial guesses  $u_0(x,t)$  and  $v_0(x,t)$  to the exact solution  $u(x,t)$  and  $v(x,t)$  of the reaction-diffusion system (1.1).

Expanding  $\phi(x,t;p)$  and  $\varphi(x,t;p)$  as a Taylor series with respect to  $p$  yields

$$\phi(x,t;p) = u_0(x,t) + \sum_{m=1}^{\infty} u_m(x,t)p^m,$$

$$\varphi(x,t;p) = v_0(x,t) + \sum_{m=1}^{\infty} v_m(x,t)p^m,$$

where

$$u_m(x,t) = \frac{1}{m!} \frac{\partial^m \phi(x,t;p)}{\partial p^m} \Big|_{p=0}, \quad (2.3)$$

$$v_m(x,t) = \frac{1}{m!} \frac{\partial^m \varphi(x,t;p)}{\partial p^m} \Big|_{p=0}. \quad (2.4)$$

Note that if  $p = 1$

$$\phi(x,t;1) = u(x,t) = u_0(x,t) + \sum_{m=1}^{\infty} u_m(x,t), \quad (2.5)$$

$$\varphi(x, t; 1) = v(x, t) = v_0(x, t) + \sum_{m=1}^{\infty} v_m(x, t), \quad (2.6)$$

which must be one of the solutions of strongly coupled reaction-diffusion system (1.1). According to the definitions (2.3) and (2.4), the governing equation for the unknowns can be deduced from the (zero-order deformation) equations (2.1) and (2.2). For further analysis, the vectors

$$\vec{u}_n(x, t) = \{u_0(x, t), u_1(x, t), \dots, u_n(x, t)\},$$

$$\vec{v}_n(x, t) = \{v_0(x, t), v_1(x, t), \dots, v_n(x, t)\},$$

are defined.

Differentiating equations (2.1) and (2.2)  $m$ -times with respect to the parameter  $p$ , dividing by  $m!$  and setting  $p = 0$ , gives the linear equations

$$\mathcal{L}_u[u_m(x, t) - \chi_m u_{m-1}(x, t)] = \hbar R_{1m}(\vec{u}_{m-1}), \quad (2.7)$$

$$\mathcal{L}_v[v_m(x, t) - \chi_m v_{m-1}(x, t)] = \hbar R_{2m}(\vec{v}_{m-1}), \quad (2.8)$$

with the initial condition

$$u_m(x, 0) = 0 \quad v_m(x, 0) = 0,$$

where

$$R_{1m}(\vec{u}_{m-1}) = (u_{m-1})_t - a(u_{m-1})_{xx} - F(u_{m-1}, v_{m-1}), \quad (2.9)$$

$$R_{2m}(\vec{v}_{m-1}) = (v_{m-1})_t - b(u_{m-1})_{xx} - d(v_{m-1})_{xx} - G(u_{m-1}, v_{m-1}), \quad (2.10)$$

and so

$$\chi_m = \begin{cases} 0 & m \leq 1, \\ 1 & m > 1. \end{cases}$$

In (2.9) and (2.10),  $F$  and  $G$  are, in general, nonlinear functions of  $u_{m-1}$  and  $v_{m-1}$ . However, if they are linear functions then

$$F(u_{m-1}, v_{m-1}) = f(u_{m-1}, v_{m-1}),$$

$$G(u_{m-1}, v_{m-1}) = g(u_{m-1}, v_{m-1}).$$

In which case, the solution of the  $m$ -order deformation equations (2.7) and (2.8) for  $m \geq 1$  now becomes

$$u_m(x, t) = \chi_m u_{m-1}(x, t) + \hbar \int_0^t R_{1m}(\vec{u}_{m-1}) dt, \quad (2.11)$$

$$v_m(x, t) = \chi_m v_{m-1}(x, t) + \hbar \int_0^t R_{2m}(\vec{v}_{m-1}) dt. \quad (2.12)$$

Detailed analysis of the convergence of the HAM is discussed by Liao in [14]. We note that the HAM only utilizes the initial condition and makes no use of the boundary conditions.

### 3 Illustrative example

In this section, the HAM will be demonstrated on an example of a strongly coupled reaction-diffusion system (1.1). For our numerical computation, let the expression

$$\psi_m(x, t) = \sum_{k=0}^{m-1} u_k(x, t), \quad (3.1)$$

denote the  $m$ -term HAM approximation to  $u(x, t)$ . We compare the approximate analytical solution obtained using HAM for our strongly coupled reaction-diffusion system (1.1) with the known exact solution. We define  $E_m(x, t)$  to be the absolute error between the exact solution and  $m$ -term approximate HAM solution  $\psi_m(x, t)$  as follows

$$E_m(x, t) = |u(x, t) - \psi_m(x, t)|. \quad (3.2)$$

#### Example:

In this section, we present a strongly coupled reaction-diffusion system (1.1) with analytical solution to show the capability and efficiency of the HAM method described in the section 2. We consider the system (1.1) with  $a = b = d = 1$ ,  $f(u, v) = (2\pi^2 - 1)u - 2\pi^2v$  and  $g(u, v) = -v$  and initial condition as follows [7]

$$u(x, 0) = \sin^2 \pi x, \quad v(x, 0) = \cos^2 \pi x, \quad (3.3)$$

and boundary conditions as follows

$$\begin{aligned} u_x(0, t) &= u_x(1, t) = 0, \\ v_x(0, t) &= v_x(1, t) = 0. \end{aligned}$$

It can be verified that the following are the exact solutions

$$u(x, t) = e^{-t} \sin^2 \pi x, \quad v(x, t) = e^{-t} \cos^2 \pi x.$$

According to section 2, we can define two operators as

$$N_1[\phi(x, t; p)] = \frac{\partial \phi(x, t; p)}{\partial t} - \frac{\partial^2 \phi(x, t; p)}{\partial x^2} - (2\pi^2 - 1)\phi(x, t; p) + 2\pi^2 \varphi(x, t; p),$$

$$N_2[\varphi(x, t; p)] = \frac{\partial \varphi(x, t; p)}{\partial t} - \frac{\partial^2 \varphi(x, t; p)}{\partial x^2} - \frac{\partial^2 \varphi(x, t; p)}{\partial x^2} + \varphi(x, t; p).$$

Thus, we can easily obtain the zeroth-deformation equations (2.7) and (2.8) that is

$$R_{1m}(\vec{u}_{m-1}) = (u_{m-1})_t - (u_{m-1})_{xx} - (2\pi^2 - 1)u_{m-1} + 2\pi^2 v_{m-1}, \quad (3.4)$$

$$R_{2m}(\vec{v}_{m-1}) = (v_{m-1})_t - (u_{m-1})_{xx} - (v_{m-1})_{xx} + v_{m-1}. \quad (3.5)$$

We start with the initial conditions (3.3). By means of the (2.11) and (2.12), we obtain directly the other components of the HAM in the series forms of (2.5) and (2.6). Thus

$$\begin{aligned} u(x, t) &= \sin^2 \pi x + \frac{1}{180} \hbar^2 t \left( 720(1 + \hbar)^4 + 360(1 + \hbar)^3(1 + 5\hbar)t \right. \\ &\quad \left. + 240(1 + \hbar)^2(2 + 5\hbar)t^2 + 60\hbar^2(1 + \hbar)(3 + 5\hbar)t^3 \right. \\ &\quad \left. + 6\hbar^3(4 + 5\hbar)t^4 + \hbar^4 t^5 \right) \sin^2 \pi x + \frac{1}{1680} \hbar^2 t \left( 5040(1 + \hbar)^5 + \dots \right), \end{aligned}$$

and

$$v(x, t) = \cos^2 \pi x + \frac{1}{180} \hbar^2 t \left( 720(1 + \hbar)^4 + 360(1 + \hbar)^3(1 + 5\hbar)t \right. \\ \left. + 240(1 + \hbar)^2(2 + 5\hbar)t^2 + 60\hbar^2(1 + \hbar)(3 + 5\hbar)t^3 + \right. \\ \left. 6\hbar^3(4 + 5\hbar)t^4 + \hbar^4 t^5 \right) \cos^2 \pi x + \frac{1}{1680} \hbar^2 t \left( 5040(1 + \hbar)^5 + \dots \right).$$

Table 1 and 2 show absolute error between solution obtained using HAM with ten terms and the exact solution for  $u$  and  $v$ , respectively, for  $\hbar = -1$ . Cao and Sun [7] solved this system using the finite difference approximation. This shows the importance of the HAM. The solution of the strongly coupled reaction-diffusion system using HAM is more effective than the finite difference scheme. While using the HAM, the difficulty of calculating using the finite difference method does not occur.

Table 1: Absolute error  $E_{10}$  for variables  $x, t \in (0, 1)$  for  $u(x, t)$  at  $\hbar = -1$ .

$x/t$	0.1	0.3	0.7	1
0.1	$1.38778 \times 10^{-17}$	$3.05311 \times 10^{-16}$	$2.61739 \times 10^{-12}$	$1.85047 \times 10^{-10}$
0.3	$6.66134 \times 10^{-16}$	$7.77156 \times 10^{-16}$	$1.79366 \times 10^{-11}$	$1.26833 \times 10^{-9}$
0.5	$2.22045 \times 10^{-16}$	$3.21965 \times 10^{-15}$	$2.74093 \times 10^{-11}$	$1.93784 \times 10^{-9}$
0.6	$1.33227 \times 10^{-16}$	$7.99361 \times 10^{-15}$	$2.48030 \times 10^{-11}$	$1.75281 \times 10^{-9}$
0.9	$9.71445 \times 10^{-17}$	$8.32667 \times 10^{-17}$	$2.61675 \times 10^{-12}$	$1.85046 \times 10^{-10}$

Table 2: Absolute error  $E_{10}$  for variables  $x, t \in (0, 1)$  for  $v(x, t)$  at  $\hbar = -1$ .

$x/t$	0.1	0.3	0.7	1
0.1	$6.66134 \times 10^{-16}$	$2.99760 \times 10^{-15}$	$2.47903 \times 10^{-11}$	$1.75279 \times 10^{-9}$
0.3	$2.77556 \times 10^{-16}$	$1.11022 \times 10^{-15}$	$9.46906 \times 10^{-12}$	$6.69506 \times 10^{-10}$
0.6	$6.93889 \times 10^{-17}$	$3.19189 \times 10^{-16}$	$2.61718 \times 10^{-12}$	$1.85047 \times 10^{-10}$
0.8	$4.44089 \times 10^{-16}$	$2.10942 \times 10^{-15}$	$1.79385 \times 10^{-11}$	$1.26833 \times 10^{-9}$
1	$6.66134 \times 10^{-16}$	$3.21965 \times 10^{-15}$	$2.74075 \times 10^{-11}$	$1.93784 \times 10^{-9}$

Figures 1 and 2 shows the absolute error between the solution obtained using HAM with ten terms and the exact solution for  $u$  at  $t = 1$  with  $\hbar = -1$  and  $\hbar = -0.92$ , respectively. Figures 3 and 4 show the absolute error between solution obtained using HAM with ten terms and the exact solution for  $v$  at  $t = 1$  with  $\hbar = -1$  and  $\hbar = -0.92$ , respectively.

Figures 5 and 6 show the  $\hbar$ -curve for various derivatives of  $u$  and  $v$ , respectively, which shows the rate of convergence of the HAM. This shows that the solution obtained using HAM converges to the exact solution, whenever  $-1.35 \leq \hbar \leq -0.55$ .

In the figures 1-6, we have investigated a numerical solution of a strongly coupled reaction-diffusion system. It is clear that the absolute error between solution obtained using HAM and the exact solution is very small and this can be seen in the figures 1-4. We can obtain better results with a change of  $\hbar$  in the interval  $[-1.35, -0.55]$ . For example, it was shown that the results with  $\hbar = -0.92$  is

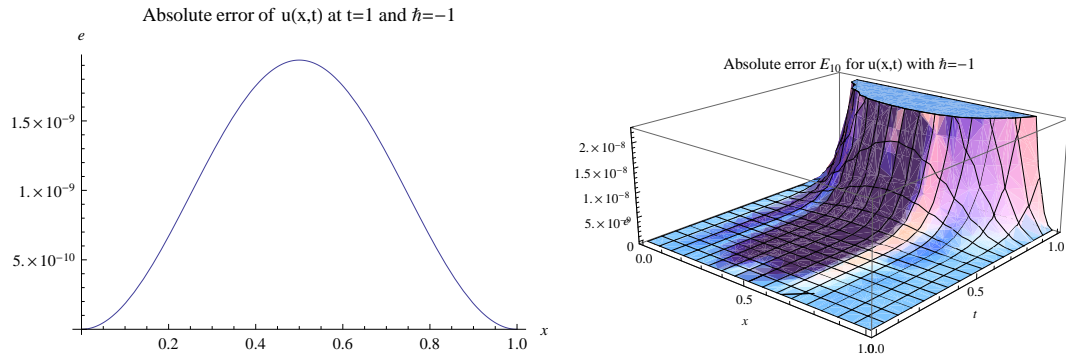


Figure 1: The left figure shows the absolute error of solution obtained using HAM with ten terms at  $t = 1$  and  $\hbar = -1$ , while the right figure shows the space-time graph of the absolute error of the exact solution  $u(x, t)$ .

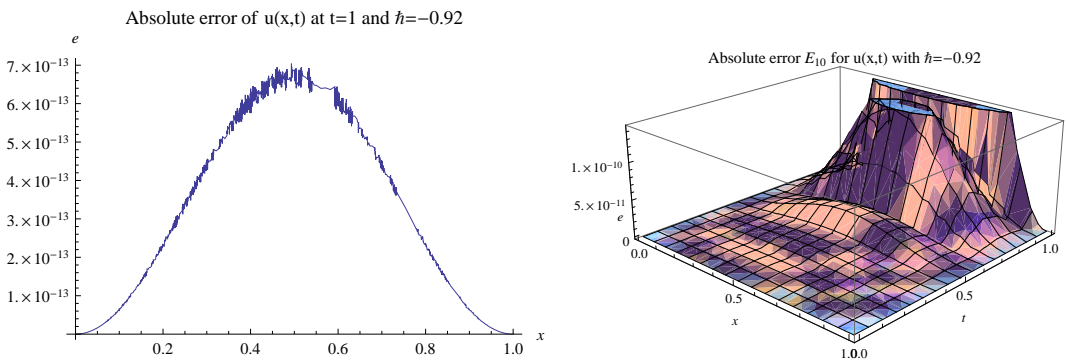


Figure 2: The left figure shows the absolute error error of solution obtained using HAM with ten terms at  $t = 1$  and  $\hbar = -0.92$ , while the right figure shows the space-time graph of the absolute error of the exact solution  $u(x, t)$ .

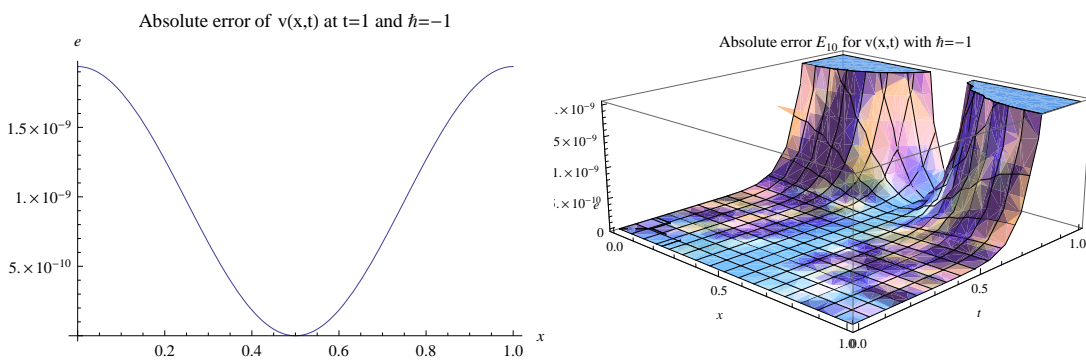


Figure 3: The left figure shows the absolute error of solution obtained using HAM with ten terms at  $t = 1$  and  $\hbar = -1$ , while the right figure shows the space-time graph of the absolute error of the exact solution  $v(x, t)$ .

better than the results with  $\hbar = -1$ . This shows the importance, effectively and capability of HAM for solving our problem. Figure 5 shows that, if we use  $u_{tt}$ ,

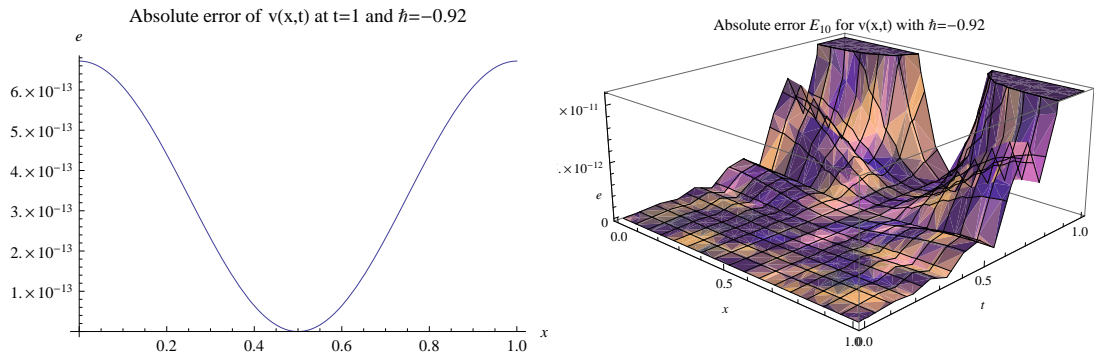


Figure 4: The left figure shows the absolute error of solution obtained using HAM with ten terms at  $t = 1$  and  $\hbar = -0.92$ , while the right figure shows the space-time graph of the absolute error of the exact solution  $v(x, t)$ .

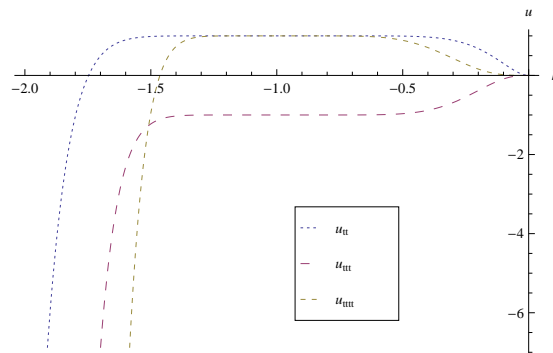


Figure 5: The  $\hbar$ -curve for various derivatives of  $u(x, t)$  at point of  $(0.5, 0)$  obtained tenth-order HAM approximation of example.

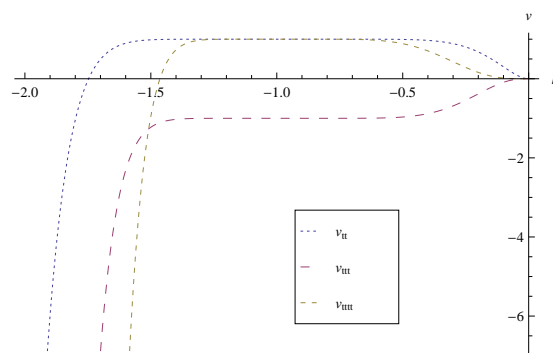


Figure 6: The  $\hbar$ -curve for various derivatives of  $v(x, t)$  at point of  $(0, 0)$  obtained tenth-order HAM approximation of example.

$u_{ttt}$  and  $u_{tttt}$  the rate of convergence of  $\hbar$  is the same and these changes does not effect in the rate of convergence.



## 4 Conclusion

In this paper, we have illustrated how Homotopy Analysis Method (HAM) can be used to solve in an approximate analytical manner the strongly coupled reaction-diffusion system. The results of an example is presented and only ten terms are required to obtain a very accurate solution. An important advantage of the HAM is that it can solve linear or nonlinear partial differential equations without any need for discretization, perturbation, transformation or linearization and it only requires the initial condition. The method was tested on one example of a strongly coupled reaction-diffusion system and it was demonstrated that the HAM is highly accurate and rapidly convergent. A disadvantage of the HAM is that this method cannot always guarantee the convergence of approximate series [13, 26] and the method depend on choosing proper linear operator and initial guesses.

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